

PCT09

## RAW SEQUENCE LISTING

DATE: 01/14/2002

PATENT APPLICATION: US/09/889,314

TIME: 13:39:58

Input Set : A:\1990035b.app

Output Set: N:\CRF3\01142002\I889314.raw

3 <110> APPLICANT: BURNIE, JAMES PETER  
 4 MATTHEWS, RUTH CHRISTINE  
 6 <120> TITLE OF INVENTION: MEDICAMENT  
 8 <130> FILE REFERENCE: 050885-0281578  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/889,314  
 C--> 11 <141> CURRENT FILING DATE: 2001-11-20  
 W--> 13-~~140~~ CURRENT APPLICATION NUMBER: GB 9902555.3  
 C--> 14-~~141~~ CURRENT FILING DATE: 1999-02-05  
 16 <150> PRIOR APPLICATION NUMBER: 09/889,314  
 17 <151> PRIOR FILING DATE: 2001-07-16  
 19 <160> NUMBER OF SEQ ID NOS: 16  
 21 <170> SOFTWARE: PatentIn Ver. 2.1  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 1491  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Chlamydia pneumoniae  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (1)..(1491)  
 32 <400> SEQUENCE: 1  
 33 gat aca aac atg tct att tca tct tct tca gga cct gac aat caa aaa 48  
 34 Asp Thr Asn Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys  
 35 1 5 10 15  
 37 aat atc atg tct caa gtt ctg aca tcg aca ccc cag ggc gtg ccc caa 96  
 38 Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln  
 39 20 25 30  
 41 caa gat aag ctg tct ggc aac gaa acg aag caa ata cag caa aca cgt 144  
 42 Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg  
 43 35 40 45  
 45 cag ggt aaa aac act gag atg gaa agc gat gcc act att gct ggt gct 192  
 46 Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala  
 47 50 55 60  
 49 tct gga aaa gac aaa act tcc tcg act aca aaa aca gaa aca gct cca 240  
 50 Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro  
 51 65 70 75 80  
 53 caa cag gga gtt gct gct ggg aaa gaa tcc tca gaa agt caa aag gca 288  
 54 Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala  
 55 85 90 95  
 57 ggt gct gat act gga gta tca gga gcg gct gct act aca gca tca aat 336  
 58 Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn  
 59 100 105 110  
 61 act gca aca aaa att gct atg cag acc tct att gaa gag gcg agc aaa 384  
 62 Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys  
 63 115 120 125  
 65 agt atg gag tct acc tta gag tca ctt caa agc ctc agt gcc gcg caa 432  
 66 Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln  
 67 130 135 140

Does Not Comply  
 Corrected Diskette Needed

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69 atg aaa gaa gtc gaa gcg gtt gtt gtt gct gcc ctc tca ggg aaa agt 480
70 Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser
71 145 150 155 160
73 tcg ggt tcc gca aaa ttg gaa aca cct gag ctc ccc aag ccc ggg gtg 528
74 Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val
75 165 170 175
77 aca cca aga tca gag gtt atc gaa atc gga ctc gcg ctt gct aaa gca 576
78 Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala
79 180 185 190
81 att cag aca ttg gga gaa gcc aca aaa tct gcc tta tct aac tat gca 624
82 Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala
83 195 200 205
85 agt aca caa gca caa gca gac caa aca aat aaa cta ggt cta gaa aag 672
86 Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys
87 210 215 220
89 caa gcg ata aaa atc gat aaa gaa cga gaa gaa tac caa gag atg aag 720
90 Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys
91 225 230 235 240
93 gct gcc gaa cag aag tct aaa gat ctc gaa gga aca atg gat act gtc 768
94 Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val
95 245 250 255
97 aat act gtg atg atc gcg gtt tct gtt gcc att aca gtt att tct att 816
98 Asn Thr Val Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile
99 260 265 270
101 gtt gct gct att ttt aca tgc gga gct gga ctc gct gga ctc gct gcg 864
102 Val Ala Ala Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala
103 275 280 285
105 gga gct gct gta ggt gca gcg gca gct gga ggt gca gca gga gct gct 912
106 Gly Ala Ala Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala
107 290 295 300
109 gcc gca acc acg gta gca aca caa att aca gtt caa gct gtt gtc caa 960
110 Ala Ala Thr Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln
111 305 310 315 320
113 gcg gtg aaa caa gct gtt atc aca gct gtc aga caa gcg atc acc gcg 1008
114 Ala Val Lys Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala
115 325 330 335
117 gct ata aaa gcg gct gtc aaa tct gga ata aaa gca ttt atc aaa act 1056
118 Ala Ile Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr
119 340 345 350
121 tta gtc aaa gcg att gcc aaa gcc att tct aaa gga atc tct aag gtt 1104
122 Leu Val Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val
123 355 360 365
125 ttc gct aag gga act caa atg att gcg aag aac ttc ccc aag ctc tcg 1152
126 Phe Ala Lys Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser
127 370 375 380
129 aaa gtc atc tcg tct ctt acc agt aaa tgg gtc acg gtt ggg gtt ggg 1200
130 Lys Val Ile Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly
131 385 390 395 400
133 gtt gta gtt gcg gcg cct gct ctc ggt aaa ggg att atg caa atg cag 1248

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134 Val Val Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln
135          405          410          415
137 ctc tcg gag atg caa caa aac gtc gct caa ttt cag aaa gaa gtc gga 1296
138 Leu Ser Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly
139          420          425          430
141 aaa ctg cag gct gcg gct gat atg att tct atg ttc act caa ttt tgg 1344
142 Lys Leu Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp
143          435          440          445
145 caa cag gca agt aaa att gcc tca aaa caa aca ggc gag tct aat gaa 1392
146 Gln Gln Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu
147          450          455          460
149 atg act caa aaa gct acc aag ctg ggc gct caa atc ctt aaa gcg tat 1440
150 Met Thr Gln Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr
151 465          470          475          480
153 gcc gca atc agc gga gcc atc gct ggc gca cat aaa acc aat aat ttt 1488
154 Ala Ala Ile Ser Gly Ala Ile Ala Gly Ala His Lys Thr Asn Asn Phe
155          485          490          495
157 taa 1491
161 <210> SEQ ID NO: 2
162 <211> LENGTH: 496
163 <212> TYPE: PRT
164 <213> ORGANISM: Chlamydia pneumoniae
166 <400> SEQUENCE: 2
167 Asp Thr Asn Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys
168 1 5 10 15
170 Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln
171 20 25 30
173 Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg
174 35 40 45
176 Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala
177 50 55 60
179 Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro
180 65 70 75 80
182 Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala
183 85 90 95
185 Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Thr Thr Ala Ser Asn
186 100 105 110
188 Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys
189 115 120 125
191 Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln
192 130 135 140
194 Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser
195 145 150 155 160
197 Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val
198 165 170 175
200 Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala
201 180 185 190
203 Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala
204 195 200 205

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```

206 Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys
207      210                      215                      220
209 Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys
210 225                      230                      235                      240
212 Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val
213                      245                      250                      255
215 Asn Thr Val Met Ile Ala Val Ser Val Ala Ile Thr Val Ile Ser Ile
216                      260                      265                      270
218 Val Ala Ala Ile Phe Thr Cys Gly Ala Gly Leu Ala Gly Leu Ala Ala
219                      275                      280                      285
221 Gly Ala Ala Val Gly Ala Ala Ala Ala Gly Gly Ala Ala Gly Ala Ala
222      290                      295                      300
224 Ala Ala Thr Thr Val Ala Thr Gln Ile Thr Val Gln Ala Val Val Gln
225 305                      310                      315                      320
227 Ala Val Lys Gln Ala Val Ile Thr Ala Val Arg Gln Ala Ile Thr Ala
228                      325                      330                      335
230 Ala Ile Lys Ala Ala Val Lys Ser Gly Ile Lys Ala Phe Ile Lys Thr
231                      340                      345                      350
233 Leu Val Lys Ala Ile Ala Lys Ala Ile Ser Lys Gly Ile Ser Lys Val
234                      355                      360                      365
236 Phe Ala Lys Gly Thr Gln Met Ile Ala Lys Asn Phe Pro Lys Leu Ser
237      370                      375                      380
239 Lys Val Ile Ser Ser Leu Thr Ser Lys Trp Val Thr Val Gly Val Gly
240 385                      390                      395                      400
242 Val Val Val Ala Ala Pro Ala Leu Gly Lys Gly Ile Met Gln Met Gln
243                      405                      410                      415
245 Leu Ser Glu Met Gln Gln Asn Val Ala Gln Phe Gln Lys Glu Val Gly
246                      420                      425                      430
248 Lys Leu Gln Ala Ala Ala Asp Met Ile Ser Met Phe Thr Gln Phe Trp
249      435                      440                      445
251 Gln Gln Ala Ser Lys Ile Ala Ser Lys Gln Thr Gly Glu Ser Asn Glu
252      450                      455                      460
254 Met Thr Gln Lys Ala Thr Lys Leu Gly Ala Gln Ile Leu Lys Ala Tyr
255 465                      470                      475                      480
257 Ala Ala Ile Ser Gly Ala Ile Ala Gly Ala His Lys Thr Asn Asn Phe
258                      485                      490                      495
261 <210> SEQ ID NO: 3
262 <211> LENGTH: 302
263 <212> TYPE: PRT
264 <213> ORGANISM: Artificial Sequence
266 <220> FEATURE:
267 <223> OTHER INFORMATION: Description of Artificial Sequence: Codon
268      optimised N-terminal section of Chlamydia
269      pneumoniae protein
271 <220> FEATURE:
272 <221> NAME/KEY: UNSURE
273 <222> LOCATION: (1)..(30)
274 <223> OTHER INFORMATION: S-tag and thrombin cleavage site
276 <220> FEATURE:

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277 &lt;223&gt; OTHER INFORMATION: Positions (297)..(302) comprise Histidine tag

279 &lt;400&gt; SEQUENCE: 3

280 Met Lys Glu Thr Ala Ala Ala Lys Phe Glu Arg Gln His Met Asp Ser

281 1 5 10 15

283 Pro Asp Leu Gly Thr Leu Val Pro Arg Gly Ser Ala Ile Ser Asp Pro

284 20 25 30

286 Asp Thr Asn Met Ser Ile Ser Ser Ser Ser Gly Pro Asp Asn Gln Lys

287 35 40 45

289 Asn Ile Met Ser Gln Val Leu Thr Ser Thr Pro Gln Gly Val Pro Gln

290 50 55 60

292 Gln Asp Lys Leu Ser Gly Asn Glu Thr Lys Gln Ile Gln Gln Thr Arg

293 65 70 75 80

295 Gln Gly Lys Asn Thr Glu Met Glu Ser Asp Ala Thr Ile Ala Gly Ala

296 85 90 95

298 Ser Gly Lys Asp Lys Thr Ser Ser Thr Thr Lys Thr Glu Thr Ala Pro

299 100 105 110

301 Gln Gln Gly Val Ala Ala Gly Lys Glu Ser Ser Glu Ser Gln Lys Ala

302 115 120 125

304 Gly Ala Asp Thr Gly Val Ser Gly Ala Ala Ala Thr Thr Ala Ser Asn

305 130 135 140

307 Thr Ala Thr Lys Ile Ala Met Gln Thr Ser Ile Glu Glu Ala Ser Lys

308 145 150 155 160

310 Ser Met Glu Ser Thr Leu Glu Ser Leu Gln Ser Leu Ser Ala Ala Gln

311 165 170 175

313 Met Lys Glu Val Glu Ala Val Val Val Ala Ala Leu Ser Gly Lys Ser

314 180 185 190

316 Ser Gly Ser Ala Lys Leu Glu Thr Pro Glu Leu Pro Lys Pro Gly Val

317 195 200 205

319 Thr Pro Arg Ser Glu Val Ile Glu Ile Gly Leu Ala Leu Ala Lys Ala

320 210 215 220

322 Ile Gln Thr Leu Gly Glu Ala Thr Lys Ser Ala Leu Ser Asn Tyr Ala

323 225 230 235 240

325 Ser Thr Gln Ala Gln Ala Asp Gln Thr Asn Lys Leu Gly Leu Glu Lys

326 245 250 255

328 Gln Ala Ile Lys Ile Asp Lys Glu Arg Glu Glu Tyr Gln Glu Met Lys

329 260 265 270

331 Ala Ala Glu Gln Lys Ser Lys Asp Leu Glu Gly Thr Met Asp Thr Val

332 275 280 285

334 Asn Thr Val Ala Ala Ala Leu Glu His His His His His His

335 290 295 300

338 &lt;210&gt; SEQ ID NO: 4

339 &lt;211&gt; LENGTH: 9

340 &lt;212&gt; TYPE: PRT

341 &lt;213&gt; ORGANISM: Chlamydia pneumoniae

343 &lt;400&gt; SEQUENCE: 4

344 Ser Ala Lys Leu Glu Thr Pro Glu Leu

345 1 5

348 &lt;210&gt; SEQ ID NO: 5

349 &lt;211&gt; LENGTH: 7

## VERIFICATION SUMMARY

PATENT APPLICATION: US/09/889,314

DATE: 01/14/2002

TIME: 13:39:59

Input Set : A:\1990035b.app

Output Set: N:\CRF3\01142002\I889314.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:13 M:280 W: Numeric Identifier already exists, <140> found multiple times  
L:13 M:281 W: Numeric Fields not Ordered, <140> not ordered!.  
L:13 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:14 M:280 W: Numeric Identifier already exists, <141> found multiple times  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date